

# Genome Sequence of *Leuconostoc pseudomesenteroides* Strain 4882, Isolated from a Dairy Starter Culture

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**The nonstarter lactic acid bacterium *Leuconostoc pseudomesenteroides* is a species widely found in the dairy industry and plays a key role in the formation of aromatic compounds. Here, we report the first genome sequence of a dairy strain of *Leuconostoc pseudomesenteroides*, which is 2 Mb.**

*Leuconostoc pseudomesenteroides* is widely present in fermented foods, such as meat, cacao beans, kimchi, olives, wine, and fermented dairy products (2, 5–9). In dairy technology, strains of *Leuconostoc pseudomesenteroides* are found in natural mesophilic starter cultures, in association with lactococci and *Leuconostoc mesenteroides*. Its presence is beneficial for numerous technological aspects. Heterofermentative metabolism of *Leuconostoc pseudomesenteroides* produces gas (CO<sub>2</sub>), allowing openness in cheese and the colonization of *Penicillium roqueforti* in blue-veined cheese. It also produces dextrans, which contribute to the texture and taste perception by increasing viscosity and to the final stability of the products (3). Finally, they produce aromatic compounds, such as diacetyl, acetaldehyde, and acetoin, which contribute to the organoleptic properties of many dairy products (4, 8, 11).

The complete genome sequence of *Leuconostoc pseudomesenteroides* strain 4882 was determined by Roche 454 GS (FLX System) pyrosequencing performed at Eurofins Genomics (Germany). A total of 284,861 reads, totaling ~157 Mb, were obtained, providing 25-fold coverage of the genome. The reads were assembled by using Celera software, and Consed software was used for final assembly. A total of 106 large contigs ranging from 978 to 92,568 bp in size were generated and annotated on the RAST server (1).

The draft genome of *Leuconostoc pseudomesenteroides* strain 4882 is composed of 2,008,587 bp, with an average G+C content of 39%. It contains 2,086 predicted open reading frames (ORFs) covering 86.3% (1,734,651 bp) of the genome. A total of 1,454 (73.3%) putative protein-coding genes were annotated as encoding proteins with known functions. Fifty-eight predicted tRNAs were found. Twenty-four phage-related genes were found (1.3% of the genome), but no complete prophage could be identified.

There are 266 RAST subsystems represented in the genome, including genes involved in central carbohydrate, fermentation metabolism, and protein and amino acid metabolism. Analysis of the chromosome of *Leuconostoc pseudomesenteroides* strain 4882 revealed the presence of the complete set of genes involved in citrate metabolism, a key pathway in production of aromatic compounds (10).

Comparative genomics with the genome sequence of *Leuconostoc pseudomesenteroides* strain 4882 and of the type strain KCTC3652 (5) will contribute to our understanding of the adaptation of this species to fermented foods.

**Nucleotide sequence accession number.** The complete genome sequence of *Leuconostoc pseudomesenteroides* strain 4882 has been deposited at GenBank under accession number [CAKV00000000](https://www.ncbi.nlm.nih.gov/nuclot/CAKV00000000).

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